



**caBIG™** cancer Biomedical  
Informatics Grid™



# caARRAY Interoperability Review Presentation to V/CDE Workspace

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**SAIC** From Science to Solutions™

**NATIONAL  
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Center for Bioinformatics

# caARRAY

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# caARRAY

- microarray database system which has been designed, architected and constructed to be compliant with international standardization efforts in the field of microarray and gene expression-related information persistence and processing



# caARRAY

- MAGE

- MicroArray and GeneExpression Object Model and Markup Language
- 1.1 (October 2003)
- <http://www.omg.org/docs/formal/03-10-01.pdf>

- MIAME

- Minimum Information About a Microarray Experiment
- 1.1 Draft 6 (April 1, 2002)
- [http://www.mged.org/Workgroups/MIAME/miame\\_1.1.html](http://www.mged.org/Workgroups/MIAME/miame_1.1.html)



# caARRAY

- strives for Interoperability (syntactically and semantically) in compliance with:
  - MAGE
  - MIAME
  - caBIG



# caARRAY

- microarray database system which has been designed, architected and constructed to facilitate interoperability with
  - MAGE information providers (e.g. other microarray database systems),
  - MAGE information consumers (e.g. microarray analysis software)



# caARRAY

- Interoperability with other MAGE information providers and consumers is achieved thru well-documented interfaces:
  - MAGE-OM API (programmatically)
    - Provides fine grain search and retrieval of MAGE information from caARRAY via a caBIO-like API
  - MAGE-ML (document-based)
    - MAGE-ML import/export



# caARRAY

- strives to be interoperable<sup>1</sup> with other MAGE information providers<sup>2</sup>:
  - MAGE Databases/Portals
    - ArrayExpress (EBI)<sup>1</sup>
    - others
  - Microarray imaging software<sup>3</sup>
    - GenePix (Molecular Devices)<sup>3</sup>
    - GCOS (Affymetrix)<sup>1, 3</sup>
    - Imagen (BioDiscovery)<sup>3</sup>
    - others

<sup>1</sup> document based via MAGE-ML    <sup>2</sup> outside caBIG    <sup>3</sup> support for native file formats



# caARRAY

- strives to be interoperable<sup>1</sup> with other MAGE information consumers<sup>2</sup>:
  - Microarray analysis software
    - caWorkBench (Columbia University)<sup>2</sup>
    - webGenome (RTI)<sup>2</sup>
    - others

<sup>1</sup> programmatically via MAGE-OM API    <sup>2</sup> in caBIG



# caWorkBench

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caWorkBench2.0 - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Home Search Favorites Media Print Mail

Address <http://amdec-bioinfo.cu-genome.org/html/caWorkBench.htm> Go

**MDeC Bioinformatics Core Facility**  
at the Columbia Genome Center

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- Using the Facility
- Hardware
- Software
- Databases
- Staff

**Services for Users**

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**Resources**

- caWorkBench3.0
- Algorithm Reference
- Tutorials & Examples
- Links
- Maps & Directions
- Contact Us

**caWorkBench2.0 - A Platform for Integrated Genomics**

[Introduction](#) [Features](#) [Installation Requirements](#) [Application Download](#) [Sample Data](#) [Documentation and Support](#) [Video Tutorials](#)

**Introduction**

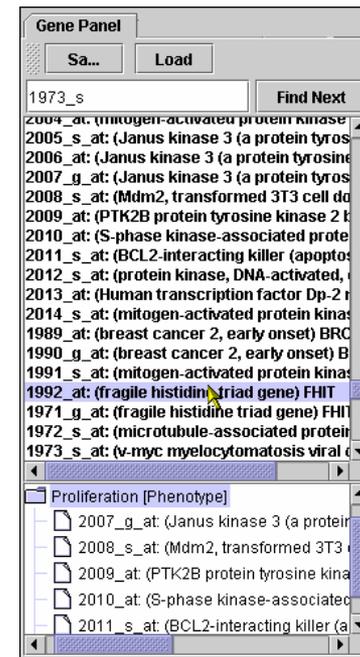
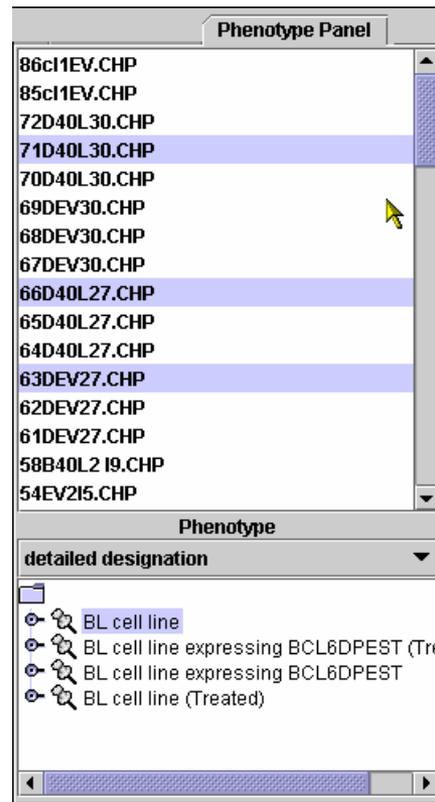
caWorkBench2.0, an open source bioinformatics platform written in Java, makes sophisticated tools for data management, analysis and visualization available to the community in a convenient fashion. It evolved from a project which was originally sponsored by the National Cancer Institute Center for Bioinformatics (NCICB). Some of the most fully developed capabilities of the platform include microarray data analysis, pathway analysis and reverse engineering, sequence analysis, transcription factor binding site analysis, and pattern discovery.

The focus in caWorkBench2.0 is on data and algorithm integration. As a result, caWorkBench2.0 users will be naturally able to combine the analysis in over 50 available caWorkBench2.0 components using a



# caWorkBench

## Data Management



# caWorkBench

The screenshot displays the caWorkBench software interface, which is used for analyzing gene expression data. The interface is divided into several panels:

- Color Mosaic:** A heatmap showing gene expression levels across different samples. The color scale ranges from red (low expression) to green (high expression). A mouse cursor is visible over the heatmap.
- Go Term Panel:** A hierarchical tree structure showing gene ontology terms. The selected term is "feeding behavior (17)". Other terms include "adult behavior(0)", "behavioral fear response(0)", "behavioral response to water deprivation(0)", "chemosensory behavior(2)", "grooming behavior(0)", "larval behavior(0)", "learning and/or memory(11)", "locomotory behavior(5)", "mechanosensory behavior(2)", "reproductive behavior(0)", "rhythmic behavior(3)", and "thermosensory behavior(0)".
- Dendrogram:** A hierarchical clustering diagram showing the relationship between samples. The samples are labeled with gene IDs such as AFX-MurL1\_2, AFX-MurL10\_2, AFX-MurL14\_2, AFX-MurFA5\_2, AFX-BoB-1\_2, AFX-BoB-2\_2, AFX-BoC-1\_2, AFX-BoC-2\_2, AFX-BoC-3\_2, AFX-BoD-1\_2, AFX-BoD-2\_2, AFX-BoD-3\_2, AFX-CeX-1\_2, AFX-CeX-2\_2, AFX-Heu-0\_2, AFX-DqX-1\_2, AFX-DqX-2\_2, AFX-LyxX-1\_2, AFX-LyxX-2\_2, AFX-PreX-1\_2, AFX-PreX-2\_2, AFX-PreX-3\_2, AFX-ThrX-1\_2, AFX-ThrX-2\_2, AFX-TpxX-1\_2, AFX-TpxX-2\_2, AFX-TpxX-3\_2, AFX-HUM10273AN97931\_1\_2, AFX-HUM10273AN97931\_2\_2, AFX-HUM10273AN97931\_3\_2, AFX-HUM10273AN97931\_4\_2, AFX-HUM10273AN97931\_5\_2, AFX-HUM10273AN97931\_6\_2, AFX-HUM10273AN97931\_7\_2, AFX-HUM10273AN97931\_8\_2, AFX-HUM10273AN97931\_9\_2, AFX-HUM10273AN97931\_10\_2, AFX-HUM10273AN97931\_11\_2, AFX-HUM10273AN97931\_12\_2, AFX-HUM10273AN97931\_13\_2, AFX-HUM10273AN97931\_14\_2, AFX-HUM10273AN97931\_15\_2, AFX-HUM10273AN97931\_16\_2, AFX-HUM10273AN97931\_17\_2, AFX-HUM10273AN97931\_18\_2, AFX-HUM10273AN97931\_19\_2, AFX-HUM10273AN97931\_20\_2, AFX-HUM10273AN97931\_21\_2, AFX-HUM10273AN97931\_22\_2, AFX-HUM10273AN97931\_23\_2, AFX-HUM10273AN97931\_24\_2, AFX-HUM10273AN97931\_25\_2, AFX-HUM10273AN97931\_26\_2, AFX-HUM10273AN97931\_27\_2, AFX-HUM10273AN97931\_28\_2, AFX-HUM10273AN97931\_29\_2, AFX-HUM10273AN97931\_30\_2, AFX-HUM10273AN97931\_31\_2, AFX-HUM10273AN97931\_32\_2, AFX-HUM10273AN97931\_33\_2, AFX-HUM10273AN97931\_34\_2, AFX-HUM10273AN97931\_35\_2, AFX-HUM10273AN97931\_36\_2, AFX-HUM10273AN97931\_37\_2, AFX-HUM10273AN97931\_38\_2, AFX-HUM10273AN97931\_39\_2, AFX-HUM10273AN97931\_40\_2, AFX-HUM10273AN97931\_41\_2, AFX-HUM10273AN97931\_42\_2, AFX-HUM10273AN97931\_43\_2, AFX-HUM10273AN97931\_44\_2, AFX-HUM10273AN97931\_45\_2, AFX-HUM10273AN97931\_46\_2, AFX-HUM10273AN97931\_47\_2, AFX-HUM10273AN97931\_48\_2, AFX-HUM10273AN97931\_49\_2, AFX-HUM10273AN97931\_50\_2.
- Reverse Engineering Analysis:** A network diagram showing interactions between genes. The nodes are colored (green, red, blue) and connected by lines. The selected gene is "v-myc myelocytomatosis viral oncogene homolog (avian)". The network diagram shows a complex web of interactions between various genes, with the selected gene at the center.



# webGenome

webGenome: Select Experiments - Microsoft Internet Explorer

File Edit View Favorites Tools Help Links »

webGenome

dhall logged in Logout Help

Overview Plot Data Virtual Experiments Analytic Pipelines

Data Plot Parameters Scatter Plot Annotation Plot Annotation Report Ideogram Plot Probe Plot

Select Experiments → Select Experiment Type → Select Probe Sets → Select Assembly → Mapping Completed

Select	Experiment Name	Database	Experiment Description	Contact
<input type="checkbox"/>	experiment_1	Excel	Test experiment 1	dhall@rti.org
<input type="checkbox"/>	experiment_2	Excel	Test experiment 2	dhall@rti.org
<input type="checkbox"/>	expression_data	Excel	Test experiment 1	dhall@rti.org
<input type="checkbox"/>	small_experiment	Excel	Test experiment	dhall@rti.org
<input type="checkbox"/>	Submitted by agarwal	SKY/M-FISH&CGH	SKY/M-FISH&CGH experiments submitted by agarwal	agarwal
<input type="checkbox"/>	Submitted by ajschaeffer	SKY/M-FISH&CGH	SKY/M-FISH&CGH experiments submitted by ajschaeffer	ajschaeffer
<input type="checkbox"/>	Submitted by alfhm	SKY/M-FISH&CGH	SKY/M-FISH&CGH experiments submitted by alfhm	alfhm
<input type="checkbox"/>	Submitted by difilip	SKY/M-FISH&CGH	SKY/M-FISH&CGH experiments submitted by difilip	difilip
<input type="checkbox"/>	Submitted by ohadimi	SKY/M-...	SKY/M-FISH&CGH experiments submitted by	ohadimi

Done Local intranet



```
// Initialize secure session with MAGE-OM server
```

```
SecureSession session = SecureSessionFactory.defaultSecureSession  
session.direct(sessionManagerUrl);  
session.start(userName, password);
```

```
// Set up search criteria
```

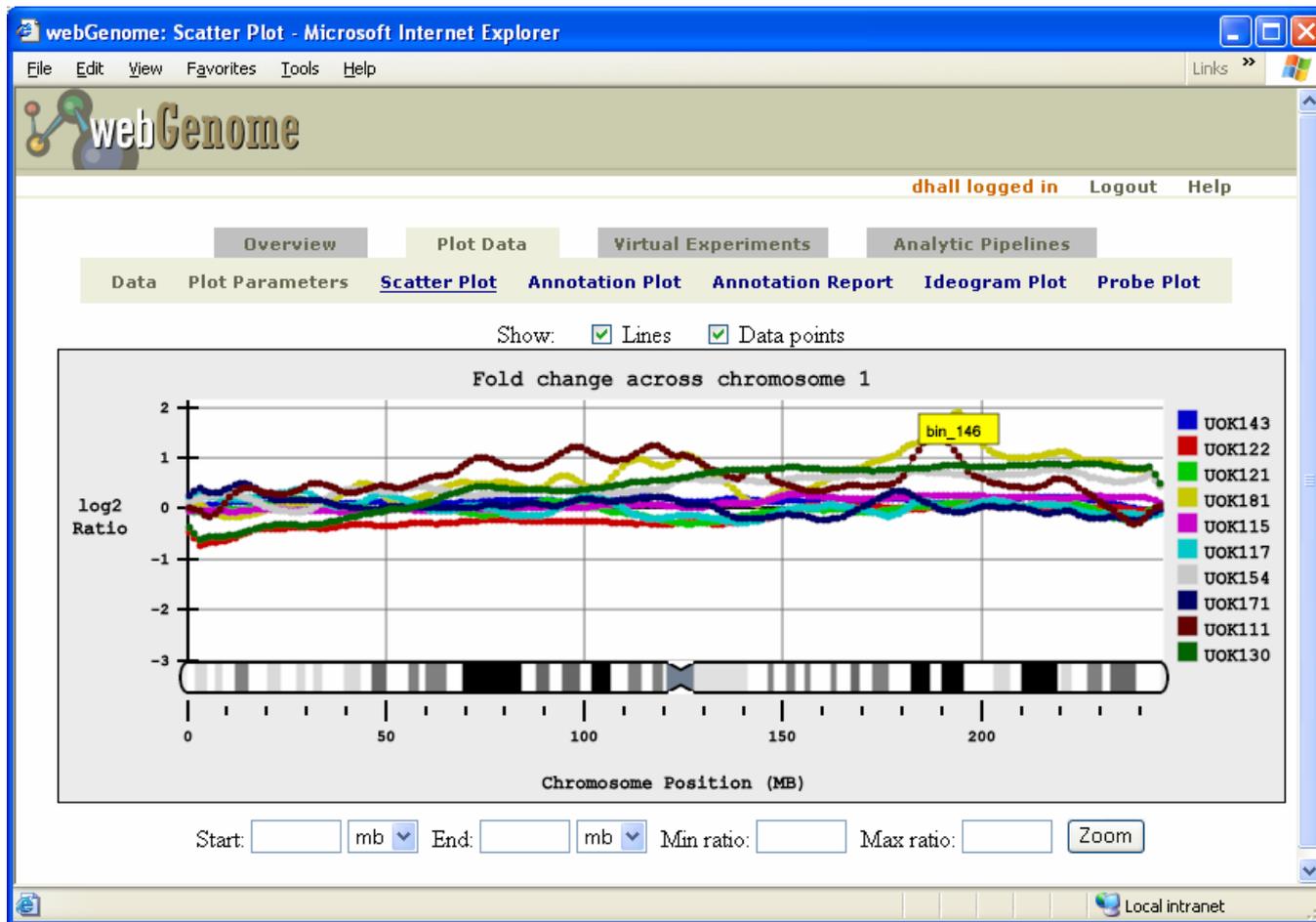
```
ExperimentSearchCriteria searchCriteria =  
    SearchCriteriaFactory.new_EXPERIMENT_EXPERIMENT_SC();  
searchCriteria.setSessionId(session);
```

```
// Perform search
```

```
SearchResult result = searchCriteria.search();  
Experiment[] experiments = (Experiment[])result.getResultSet();
```



# webGenome



# caARRAY

- allows day to day management and analysis of microarray data, and facilitates data sharing between research centers
- designed to capture MIAME 1.1 level annotations
- supports programmatic query and retrieval of gene expression data via MAGE-OM API
- supports data exchange complying with international standardized format MAGE-ML
- data can be migrated to a central caARRAY database at the NCI or caARRAY can be deployed locally at other affiliated organizations
- supports submission and retrieval of Affymetrix, GenePix, and ImaGene native format data files



# caARRAY

The screenshot shows a Microsoft Internet Explorer browser window displaying the caARRAY search protocols page. The address bar shows the URL: <http://caarraydb.nci.nih.gov/caarray/searchProtocols.do?mode=setup>. The page features the cancer.gov logo and the National Cancer Institute logo. A navigation menu includes links for HOME, CONTACTS, PROTOCOLS, ARRAYS, ONTOLOGIES, BIOMATERIALS, EXPERIMENTS, and LOGOUT. The main content area is titled "SEARCH PROTOCOLS" and contains a search form with the following fields:

SEARCH PROTOCOLS	
Protocol Type	All
Protocol Name	<input type="text"/>
Visibility	All

Buttons for Search, Reset, and Help are located at the bottom right of the search form. A left sidebar contains a "PROTOCOLS" menu with links to SEARCH HARDWARE, NEW HARDWARE, SEARCH SOFTWARE, NEW SOFTWARE, SEARCH PROTOCOLS, and NEW PROTOCOL. Below this is a "QUICK LINKS" section with links to NCI HOME, NCICB HOME, caARRAY WEBSITE, NCICB SUPPORT, HELP, and ABOUT. The footer of the page includes links for CONTACT US, PRIVACY NOTICE, DISCLAIMER, ACCESSIBILITY, and APPLICATION SUPPORT.



# caARRAY

Hybridization File Upload Hybridization Protocol - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Address <http://caarraydb.nci.nih.gov/caarray/hybridizationHybProtocol.do>

**cancer.gov**

**caARRAY** NATIONAL CANCER INSTITUTE

EXPERIMENT HOME CONTACTS PROTOCOLS ARRAYS ONTOLOGIES BIOMATERIALS EXPERIMENTS LOGOUT

IMPORT IMAGE-ML  
SEARCH/MODIFY  
NEW EXPERIMENT

QUICK LINKS  
NCI HOME  
NCICB HOME  
caARRAY WEBSITE  
NCICB SUPPORT  
HELP  
ABOUT

### COMMON HYBRIDIZATION INFORMATION

Array Design:	hg_u95av2
Number of Channels:	1
Hybridization File Type:	Affymetrix
Array Group Template Name:	U95av2-1_3

Hybridization Protocol:   
If the protocol you would like to select is not listed, you can add this protocol to the caArray database ([How?](#)).

\* indicates a required field

### PROTOCOL

Protocol ID:	gov.nih.nci.ncicb.caarray:Protocol:1015897549070016:1		
* Activity Date:	<input type="text"/>		
* Performer:	<input type="text"/>		
Protocol Name:	Affymetrix hybridization u95av2		
Protocol Description:	<input type="text"/>		
URI:	<input type="text"/>		
Protocol Parameters:	NAME	VALUE	TYPE

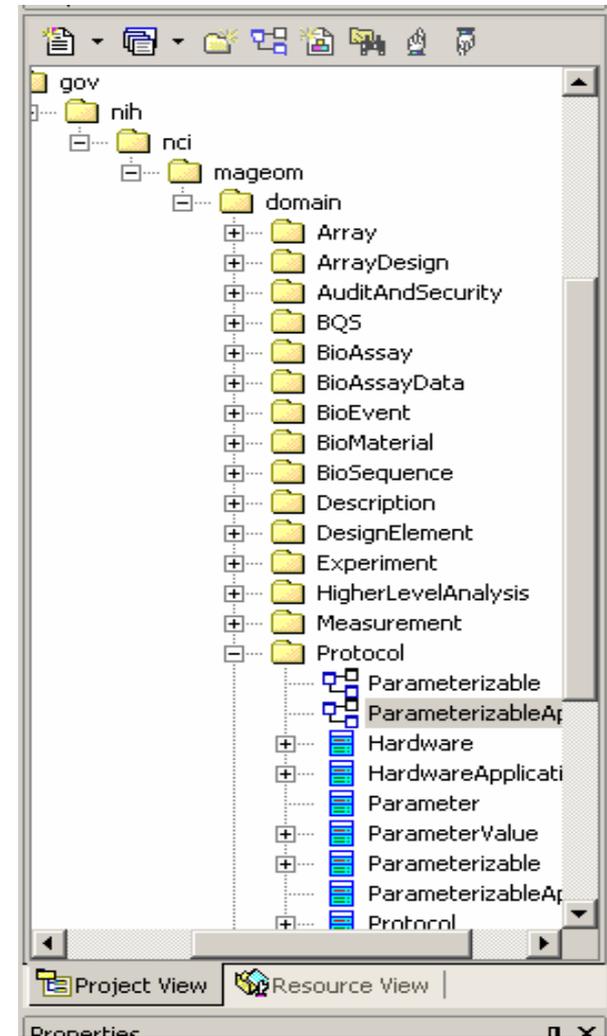
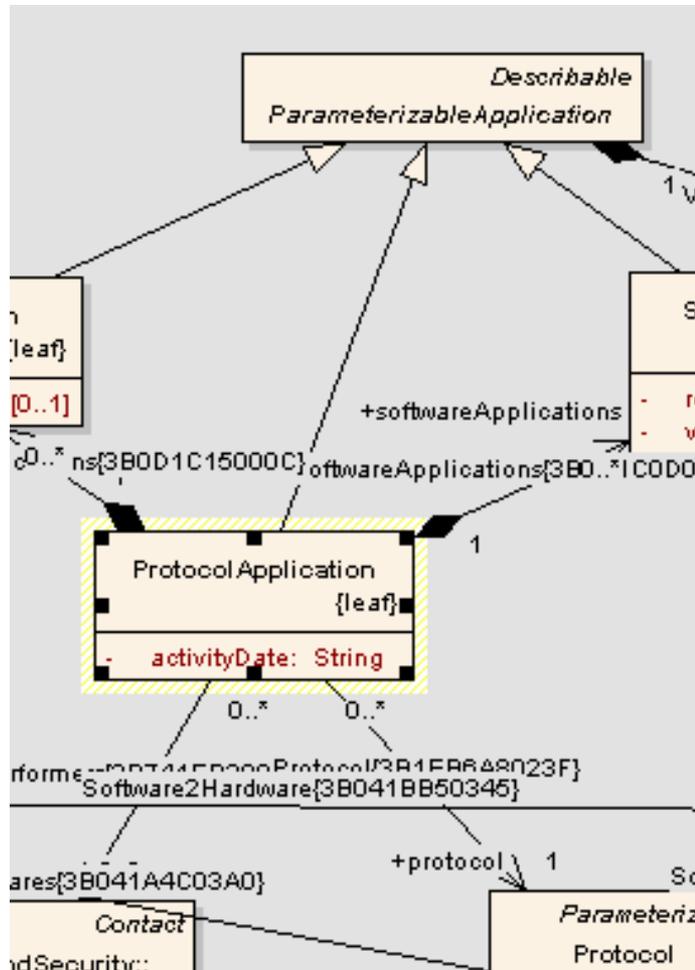
Next Cancel Help

CONTACT US PRIVACY NOTICE DISCLAIMER ACCESSIBILITY APPLICATION SUPPORT

**cancer.gov** National Institutes of Health (NIH) DEPARTMENT OF HEALTH & HUMAN SERVICES FIRST GOV Your First Click to the U.S. Government



# caARRAY



# caARRAY

**Data Element Concept - Microsoft Internet Explorer**

Address: <http://cdebrowser.nci.nih.gov/CDEBrowser/search?dataElementConceptDetails=9&tabClicked=1&PageId=GetDetailsGroup>

<b>Public ID:</b>	2236752
<b>Version:</b>	1.0
<b>Long Name:</b>	Protocol Application
<b>Preferred Name:</b>	C44184
<b>Context:</b>	caBIG
<b>Qualifier:</b>	

**Object Class Concepts**

Concept Name	Concept Code	Public ID	Definition Source	EVS Source	Primary
Protocol Application	<a href="#">C44184</a>	2236570	NCICB	NCI_CONCEPT_CODE	Yes

**Property**

<b>Public ID:</b>	2236660
<b>Version:</b>	1.0
<b>Long Name:</b>	Activity Date
<b>Preferred Name:</b>	C43431;C25164
<b>Context:</b>	caBIG
<b>Qualifier:</b>	

**Property Concepts**

Concept Name	Concept Code	Public ID	Definition Source	EVS Source	Primary
Activity	<a href="#">C43431</a>	2222740	NCI	NCI_CONCEPT_CODE	No
Date	<a href="#">C25164</a>	2202880	NCI	NCI_CONCEPT_CODE	Yes

User: Public User      Version 3.0.1.2 Build 20      Please send comments and suggestions to [ncicb@pop.nci.nih.gov](mailto:ncicb@pop.nci.nih.gov)



# caARRAY

The screenshot shows a Microsoft Internet Explorer browser window displaying the NCI Terminology Browser. The address bar shows the URL: [http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?bookmarktag=1&dictionary=NCI\\_Thesaurus&code=C43431](http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?bookmarktag=1&dictionary=NCI_Thesaurus&code=C43431). The page header includes the National Cancer Institute logo and the text "National Cancer Institute" and "U.S. National Institutes of Health | www.cancer.gov".

The main content area is titled "Concept Details" and includes a "Bookmark this page" link. The concept being viewed is "Activity", with a "Printable Page", "History", and "Graph" link. The "Identifiers" section shows the name "Activity" and the code "C43431". The "Information about this concept" section includes the following details:

Field	Value
DEFINITION	NCI The state of being active; any specific activity.
Synonym with source data	Activity PT NCI
Preferred_Name	Activity
Semantic_Type	Activity
Synonym	Activity

The "Superconcepts" section lists "Conceptual\_Entities".

At the bottom of the browser window, there is a status bar with the text "Error on page." and "Trusted sites".



# caARRAY

The screenshot shows the NCI Terminology Browser interface in Microsoft Internet Explorer. The browser window title is "NCI Terminology Browser - Microsoft Internet Explorer". The address bar shows the URL: [http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?bookmarktag=1&dictionary=NCI\\_Thesaurus&&code=C25164](http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?bookmarktag=1&dictionary=NCI_Thesaurus&&code=C25164). The page header features the National Cancer Institute logo and the text "National Cancer Institute" and "U.S. National Institutes of Health | www.cancer.gov". Below the header, there are search options: "Quick Search" and "Advanced Search". The "Advanced Search" section shows a dropdown menu with "Information about this concept" selected, and another dropdown with "Accepted\_Therapeutic\_Use\_For". There is also a "Max Results" dropdown set to "100" and a "Date" field. The main content area is titled "Concept Details" and includes a "Bookmark this page" link. A table lists various identifiers and information about the concept "Date".

Identifiers:	
name	Date
code	C25164

Information about this concept:	
DEFINITION	NCI The particular day, month and year an event happened or will happen.
Synonym with source data	DT AB CADSR
Synonym with source data	Date PT CADSR
Synonym with source data	Date PT NCI
Preferred_Name	Date
Semantic_Type	Temporal Concept
Synonym	DT
Synonym	Date
Unified Medical Language System Concept Identifier	<a href="#">C0011008</a>



# caARRAY

- strives to support existing standardization efforts and to follow caBIG guidelines to increase the probability that other software information systems can be interoperable with caARRAY



# caARRAY

- used MAGE UML model to describe caARRAY software system
- created MAGE UML class diagrams to illustrate classes, attributes, and relationships
- strived to use naming conventions and terminology standards prescribed by MAGE, MGED Society and the caBIG program
- strived to fully annotate MAGE UML model with class and attribute definitions, and with associated terminology concept codes



# caARRAY

- MAGE-OM API is well-documented
- MAGE-OM API provides information which is based upon an object-oriented abstraction of the underlying data in caARRAY
- MAGE-OM API returns data in the form of objects that are instances of classes in the UML model



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- Kevin Fitzpatrick
- John Moy
- Sharon Settnek
- Tara Akhavan



# Thanks

- caBIG community

